

SEQUENCE LISTING

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<120> Plant production of immunoglobulins with reduced fucosylation

<130> 038136-5001-US

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<160> 85

<170> PatentIn version 3.1

<210> 1

<211> 1494

<212> DNA

<213> Herpes simplex virus

<220>

<221> CDS

<222> (1)..(1494)

<220>

<221> misc_feature

<223> HSV Heavy Chain sequence

<400> 1

atg gga tgg agc tgg atc ttt ctc ttc ctc ctg tca gga gct gca ggt	48
Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Ser Gly Ala Ala Gly	
1 5 10 15	

gtc cat tgc cag gtt cag ctc gtg cag tca ggt gct gag gtg aag aag	96
Val His Cys Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
20 25 30	

cct ggc tcc tcg gtg aag gtc tcc tgc aag gct tct gga ggt tcc ttc	144
Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Ser Phe	
35 40 45	

agc tcc tat gct atc aac tgg gtg agg caa gct cct gga caa ggg ctt Ser Ser Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu 50 55 60	192
gag tgg atg gga ggg ctc atg cct atc ttt ggg aca aca aac tac gcg Glu Trp Met Gly Gly Leu Met Pro Ile Phe Gly Thr Thr Asn Tyr Ala 65 70 75 80	240
cag aag ttc cag gac agg ctc acg att acc gcg gac gta tcc acg agt Gln Lys Phe Gln Asp Arg Leu Thr Ile Thr Ala Asp Val Ser Thr Ser 85 90 95	288
aca gcc tac atg caa ctg agc ggc ctg aca tat gaa gac acg gcc atg Thr Ala Tyr Met Gln Leu Ser Gly Leu Thr Tyr Glu Asp Thr Ala Met 100 105 110	336
tat tac tgt gcg aga gtt gcc tac atg ctt gaa cct acc gtc act gca Tyr Tyr Cys Ala Arg Val Ala Tyr Met Leu Glu Pro Thr Val Thr Ala 115 120 125	384
ggc ggt ttg gac gtc tgg ggc caa ggg acc ttg gtc acc gtc tcc tcc Gly Gly Leu Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser 130 135 140	432
gca tcc ccg acc agc ccg aag gtc ttc ccg ctg agc ctc tgt agc acc Ala Ser Pro Thr Ser Pro Lys Val Phe Pro Leu Ser Leu Cys Ser Thr 145 150 155 160	480
cag cca gat ggg aac gtg gtc atc gcc tgc ctg gtc cag ggc ttc ttc Gln Pro Asp Gly Asn Val Val Ile Ala Cys Leu Val Gln Gly Phe Phe 165 170 175	528
cct cag gag cca ctc agt gtg acc tgg agc gaa agc gga cag ggc gtg Pro Gln Glu Pro Leu Ser Val Thr Trp Ser Glu Ser Gly Gln Gly Val 180 185 190	576
acc gcc agg aac ttc cca ccc agc cag gat gcc tcc gga gac ctg tac Thr Ala Arg Asn Phe Pro Pro Ser Gln Asp Ala Ser Gly Asp Leu Tyr 195 200 205	624
acc acg tcc agc cag ctg acc ctt ccg gcc aca cag tgc cta gcg ggc Thr Thr Ser Ser Gln Leu Thr Leu Pro Ala Thr Gln Cys Leu Ala Gly 210 215 220	672
aag tcc gtg aca tgc cac gtg aag cac tac acg aat ccc agc cag gat Lys Ser Val Thr Cys His Val Lys His Tyr Thr Asn Pro Ser Gln Asp 225 230 235 240	720
gtg act gtg ccc tgc cca gtt ccc tca act cca cct acc cca tct ccc Val Thr Val Pro Cys Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro 245 250 255	768
tcg act cca cct acc cca tct ccc tca tgc tgc cac ccc agg ctg tca Ser Thr Pro Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg Leu Ser 260 265 270	816

ctg cac agg cct gcc ctc gag gac ctg ctc tta ggt tcg gaa gcg aac	864
Leu His Arg Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu Ala Asn	
275 280 285	
ctc acg tgc aca ctc acc ggc ctg aga gat gcg tca ggt gtc acc ttc	912
Leu Thr Cys Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val Thr Phe	
290 295 300	
acc tgg acg ccc tca agt ggt aag agc gct gtt caa ggc cca cct gag	960
Thr Trp Thr Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro Pro Glu	
305 310 315 320	
cgt gac ctc tgt ggc tgc tac agc gtg tcc agt gtc ctt ccg ggc tgt	1008
Arg Asp Leu Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro Gly Cys	
325 330 335	
gcc gag cct tgg aat cat ggg aag acc ttc act tgc act gct gcc tac	1056
Ala Glu Pro Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr	
340 345 350	
ccc gag agc aag acc ccg cta acc gcc acc ctc tcg aaa tcc ggc aac	1104
Pro Glu Ser Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn	
355 360 365	
aca ttc cgg ccc gag gtc cac ctg ctg ccg ccg ccg tcg gag gag ctg	1152
Thr Phe Arg Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu Glu Leu	
370 375 380	
gcc ctg aac gag ctg gtg acg ctg acg tgc ctg gcg cgc ggc ttc agc	1200
Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser	
385 390 395 400	
ccc aag gac gtg ctg gtt cgc tgg ctg cag ggc tca cag gag ctg cct	1248
Pro Lys Asp Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro	
405 410 415	
agg gag aag tac ctg act tgg gca tcc ccg cag gag ccc agc caa ggc	1296
Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly	
420 425 430	
acc acc acc ttc gct gtg acc tcg ata ctg cgc gtg gca gcc gag gac	1344
Thr Thr Thr Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu Asp	
435 440 445	
tgg aag aag ggt gac acc ttc tcc tgc atg gtg ggc cac gag gcc ctt	1392
Trp Lys Lys Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala Leu	
450 455 460	
ccg ctg gcc ttc aca cag aag acc atc gac cgc ttg gcg ggt aaa ccc	1440
Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly Lys Pro	
465 470 475 480	
acc cat gtc aat gtg tct gtt gtc atg gcg gag gtg gac ggc acc tgc	1488
Thr His Val Asn Val Ser Val Val Met Ala Glu Val Asp Gly Thr Cys	
485 490 495	
tac tga	1494

Tyr

<210> 2
<211> 497
<212> PRT
<213> Herpes simplex virus

<400> 2

Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Ala Ala Gly
1 5 10 15

Val His Cys Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Ser Phe
35 40 45

Ser Ser Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

Glu Trp Met Gly Gly Leu Met Pro Ile Phe Gly Thr Thr Asn Tyr Ala
65 70 75 80

Gln Lys Phe Gln Asp Arg Leu Thr Ile Thr Ala Asp Val Ser Thr Ser
85 90 95

Thr Ala Tyr Met Gln Leu Ser Gly Leu Thr Tyr Glu Asp Thr Ala Met
100 105 110

Tyr Tyr Cys Ala Arg Val Ala Tyr Met Leu Glu Pro Thr Val Thr Ala
115 120 125

Gly Gly Leu Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
130 135 140

Ala Ser Pro Thr Ser Pro Lys Val Phe Pro Leu Ser Leu Cys Ser Thr
145 150 155 160

Gln Pro Asp Gly Asn Val Val Ile Ala Cys Leu Val Gln Gly Phe Phe
165 170 175

Pro Gln Glu Pro Leu Ser Val Thr Trp Ser Glu Ser Gly Gln Gly Val
180 185 190

Thr Ala Arg Asn Phe Pro Pro Ser Gln Asp Ala Ser Gly Asp Leu Tyr
195 200 205

Thr Thr Ser Ser Gln Leu Thr Leu Pro Ala Thr Gln Cys Leu Ala Gly
210 215 220

Lys Ser Val Thr Cys His Val Lys His Tyr Thr Asn Pro Ser Gln Asp
225 230 235 240

Val Thr Val Pro Cys Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro
245 250 255

Ser Thr Pro Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg Leu Ser
260 265 270

Leu His Arg Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu Ala Asn
275 280 285

Leu Thr Cys Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val Thr Phe
290 295 300

Thr Trp Thr Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro Pro Glu
305 310 315 320

Arg Asp Leu Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro Gly Cys
325 330 335

Ala Glu Pro Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr
340 345 350

Pro Glu Ser Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn
355 360 365

Thr Phe Arg Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu Glu Leu
370 375 380

Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser
385 390 395 400

Pro Lys Asp Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro
405 410 415

Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly
420 425 430

Thr Thr Thr Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu Asp
435 440 445

Trp Lys Lys Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala Leu
450 455 460

Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly Lys Pro
465 470 475 480

Thr His Val Asn Val Ser Val Val Met Ala Glu Val Asp Gly Thr Cys
485 490 495

Tyr

<210> 3
<211> 57
<212> DNA
<213> Artificial sequence

<220>
<223> Heavy chain signal peptide

<220>
<221> CDS
<222> (1)..(57)

<400> 3
atg gga tgg agc tgg atc ttt ctc ttc ctc ctg tca gga gct gca ggt 48
Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Ala Ala Gly
1 5 10 15

gtc cat tgc 57
Val His Cys

<210> 4
<211> 19
<212> PRT
<213> Artificial sequence

<220>
<223> Heavy chain signal peptide

<400> 4

Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Ala Ala Gly
1 5 10 15

Val His Cys

<210> 5
<211> 1368
<212> DNA
<213> Artificial sequence

<220>
<223> Mature heavy chain sequence

<220>
<221> CDS
<222> (1)..(1368)

<400> 5
cag gtt cag ctc gtg cag tca ggt gct gag gtg aag aag cct ggc tcc 48
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

tcg gtg aag gtc tcc tgc aag gct tct gga ggt tcc ttc agc tcc tat 96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Ser Phe Ser Ser Tyr
20 25 30

gct atc aac tgg gtg agg caa gct cct gga caa ggg ctt gag tgg atg 144
Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

gga ggg ctc atg cct atc ttt ggg aca aca aac tac gcg cag aag ttc 192
Gly Gly Leu Met Pro Ile Phe Gly Thr Thr Asn Tyr Ala Gln Lys Phe
50 55 60

cag gac agg ctc acg att acc gcg gac gta tcc acg agt aca gcc tac 240
Gln Asp Arg Leu Thr Ile Thr Ala Asp Val Ser Thr Ser Thr Ala Tyr
65 70 75 80

atg caa ctg agc ggc ctg aca tat gaa gac acg gcc atg tat tac tgt 288
Met Gln Leu Ser Gly Leu Thr Tyr Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95

gcg aga gtt gcc tac atg ctt gaa cct acc gtc act gca ggt ggt ttg 336
Ala Arg Val Ala Tyr Met Leu Glu Pro Thr Val Thr Ala Gly Gly Leu
100 105 110

gac gtc tgg ggc caa ggg acc ttg gtc acc gtc tcc tcc gca tcc ccg 384
Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Pro
115 120 125

acc agc ccg aag gtc ttc ccg ctg agc ctc tgt agc acc cag cca gat 432
Thr Ser Pro Lys Val Phe Pro Leu Ser Leu Cys Ser Thr Gln Pro Asp
130 135 140

ggg aac gtg gtc atc gcc tgc ctg gtc cag ggc ttc ttc cct cag gag	480
Gly Asn Val Val Ile Ala Cys Leu Val Gln Gly Phe Phe Pro Gln Glu	
145 150 155 160	
cca ctc agt gtg acc tgg agc gaa agc gga cag ggc gtg acc gcc agg	528
Pro Leu Ser Val Thr Trp Ser Glu Ser Gly Gln Gly Val Thr Ala Arg	
165 170 175	
aac ttc cca ccc agc cag gat gcc tcc gga gac ctg tac acc acg tcc	576
Asn Phe Pro Pro Ser Gln Asp Ala Ser Gly Asp Leu Tyr Thr Thr Ser	
180 185 190	
agc cag ctg acc ctt ccg gcc aca cag tgc cta gcg ggc aag tcc gtg	624
Ser Gln Leu Thr Leu Pro Ala Thr Gln Cys Leu Ala Gly Lys Ser Val	
195 200 205	
aca tgc cac gtg aag cac tac acg aat ccc agc cag gat gtg act gtg	672
Thr Cys His Val Lys His Tyr Thr Asn Pro Ser Gln Asp Val Thr Val	
210 215 220	
ccc tgc cca gtt ccc tca act cca cct acc cca tct ccc tcg act cca	720
Pro Cys Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro	
225 230 235 240	
cct acc cca tct ccc tca tgc tgc cac ccc agg ctg tca ctg cac agg	768
Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg Leu Ser Leu His Arg	
245 250 255	
cct gcc ctc gag gac ctg ctc tta ggt tcg gaa gcg aac ctc acg tgc	816
Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu Ala Asn Leu Thr Cys	
260 265 270	
aca ctc acc ggc ctg aga gat gcg tca ggt gtc acc ttc acc tgg acg	864
Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val Thr Phe Thr Trp Thr	
275 280 285	
ccc tca agt ggt aag agc gct gtt caa ggc cca cct gag cgt gac ctc	912
Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro Pro Glu Arg Asp Leu	
290 295 300	
tgt ggc tgc tac agc gtg tcc agt gtc ctt ccg ggc tgt gcc gag cct	960
Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro Gly Cys Ala Glu Pro	
305 310 315 320	
tgg aat cat ggg aag acc ttc act tgc act gct gcc tac ccc gag agc	1008
Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser	
325 330 335	
aag acc ccg cta acc gcc acc ctc tcg aaa tcc ggc aac aca ttc cg	1056
Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn Thr Phe Arg	
340 345 350	
ccc gag gtc cac ctg ctg ccg ccg ccg tcg gag gag ctg gcc ctg aac	1104
Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn	
355 360 365	
gag ctg gtg acg ctg acg tgc ctg gcg cgc ggc ttc agc ccc aag gac	1152

Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp
 370 375 380

gtg ctg gtt cgc tgg ctg cag ggc tca cag gag ctg cct agg gag aag 1200
 Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys
 385 390 395 400

tac ctg act tgg gca tcc cgg cag gag ccc agc caa ggc acc acc acc 1248
 Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly Thr Thr Thr
 405 410 415

ttc gct gtg acc tgc ata ctg cgc gtg gca gcc gag gac tgg aag aag 1296
 Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu Asp Trp Lys Lys
 420 425 430

ggc gac acc ttc tcc tgc atg gtg ggc cac gag gcc ctt ccg ctg gcc 1344
 Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala Leu Pro Leu Ala
 435 440 445

ttc aca cag aag acc atc gac cgc 1368
 Phe Thr Gln Lys Thr Ile Asp Arg
 450 455

<210> 6
 <211> 456
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Mature heavy chain sequence

<400> 6

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Ser Phe Ser Ser Tyr
 20 25 30

Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Gly Leu Met Pro Ile Phe Gly Thr Thr Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Asp Arg Leu Thr Ile Thr Ala Asp Val Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Gln Leu Ser Gly Leu Thr Tyr Glu Asp Thr Ala Met Tyr Tyr Cys
 85 90 95

Ala Arg Val Ala Tyr Met Leu Glu Pro Thr Val Thr Ala Gly Gly Leu
100 105 110

Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Pro
115 120 125

Thr Ser Pro Lys Val Phe Pro Leu Ser Leu Cys Ser Thr Gln Pro Asp
130 135 140

Gly Asn Val Val Ile Ala Cys Leu Val Gln Gly Phe Phe Pro Gln Glu
145 150 155 160

Pro Leu Ser Val Thr Trp Ser Glu Ser Gly Gln Gly Val Thr Ala Arg
165 170 175

Asn Phe Pro Pro Ser Gln Asp Ala Ser Gly Asp Leu Tyr Thr Thr Ser
180 185 190

Ser Gln Leu Thr Leu Pro Ala Thr Gln Cys Leu Ala Gly Lys Ser Val
195 200 205

Thr Cys His Val Lys His Tyr Thr Asn Pro Ser Gln Asp Val Thr Val
210 215 220

Pro Cys Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro
225 230 235 240

Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg Leu Ser Leu His Arg
245 250 255

Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu Ala Asn Leu Thr Cys
260 265 270

Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val Thr Phe Thr Trp Thr
275 280 285

Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro Pro Glu Arg Asp Leu
290 295 300

Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro Gly Cys Ala Glu Pro
305 310 315 320

Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser
325 330 335

Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn Thr Phe Arg
340 345 350

Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn
355 360 365

Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp
370 375 380

Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys
385 390 395 400

Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly Thr Thr Thr
405 410 415

Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu Asp Trp Lys Lys
420 425 430

Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala Leu Pro Leu Ala
435 440 445

Phe Thr Gln Lys Thr Ile Asp Arg
450 455

<210> 7
<211> 69
<212> DNA
<213> Artificial sequence

<220>
<223> heavy chain tailpiece

<220>
<221> CDS
<222> (1)..(69)

<400> 7
ttg gcg ggt aaa ccc acc cat gtc aat gtg tct gtt gtc atg gcg gag 48
Leu Ala Gly Lys Pro Thr His Val Asn Val Ser Val Val Met Ala Glu
1 5 10 15

gtg gac ggc acc tgc tac tga 69
Val Asp Gly Thr Cys Tyr
20

<210> 8
 <211> 22
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> heavy chain tailpiece
 <400> 8

Leu Ala Gly Lys Pro Thr His Val Asn Val Ser Val Val Met Ala Glu
 1 5 10 15

Val Asp Gly Thr Cys Tyr
 20

<210> 9
 <211> 702
 <212> DNA
 <213> Herpes simplex virus

<220>
 <221> CDS
 <222> (1)..(702)
 <220>
 <221> misc_feature
 <223> HSV light chain sequence

<400> 9
 atg gga tgg tcc tgg atc ttt ctc ttc ctt ctg tca gga gct gca ggt 48
 Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Ala Ala Gly
 1 5 10 15
 gtc cac tgc gag atc gtg ctc acg cag tct cca ggc acc ctg tct ttg 96
 Val His Cys Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu
 20 25 30
 tcg cca ggg gaa cgt gcc acc ctc tcc tgc cgg gcc agt cag tcc gtt 144
 Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val
 35 40 45
 tcc agc gcg tac ctt gcc tgg tac cag cag aag cct ggc caa gct ccc 192
 Ser Ser Ala Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
 50 55 60
 agg ctc ctc atc tat ggt gcg tcc agc agg gct act ggc att cca gac 240
 Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp
 65 70 75 80
 cgc ttc tca ggc agt ggg tct ggg aca gac ttc acg ctc acc att agc 288
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 85 90 95

agg ctg gaa cct gag gat ttt gca gtg tac tac tgt cag cag tat ggt 336
 Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly
 100 105 110

cgc tca ccc acg ttc ggc cag ggg acc aag gtg gag atc aag cgc act 384
 Arg Ser Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
 115 120 125

gtg gct gca ccg tcg gtc ttc ata ttc ccg cca tcc gat gag cag ctg 432
 Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
 130 135 140

aag tct ggc act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccg 480
 Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
 145 150 155 160

aga gag gcg aag gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt 528
 Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
 165 170 175

aac tcc caa gag tcc gtt aca gag cag gac agc aag gac agc acc tac 576
 Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
 180 185 190

agc ctc agc aac acc ttg acg ctg agc aaa gcg gac tac gag aaa cac 624
 Ser Leu Ser Asn Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
 195 200 205

aag gtc tac gcc tgc gaa gtc acc cat caa ggc ctg cgc tcg ccc gtc 672
 Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Arg Ser Pro Val
 210 215 220

aca aag agc ttc aac cgg gga gag tgt tga 702
 Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230

<210> 10
 <211> 233
 <212> PRT
 <213> Herpes simplex virus

<400> 10

Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Ala Ala Gly
 1 5 10 15

Val His Cys Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu
 20 25 30

Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val
 35 40 45

Ser Ser Ala Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95

Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly
100 105 110

Arg Ser Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
115 120 125

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
130 135 140

Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
145 150 155 160

Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
165 170 175

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
180 185 190

Ser Leu Ser Asn Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
195 200 205

Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Arg Ser Pro Val
210 215 220

Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 11
<211> 57
<212> DNA
<213> Artificial sequence

<220>
<223> Light chain signal peptide

<220>

<221> CDS
<222> (1)..(57)

<400> 11
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Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Ala Ala Gly
1 5 10 15

gtc cac tgc 57
Val His Cys

<210> 12
<211> 19
<212> PRT
<213> Artificial sequence

<220>
<223> Light chain signal peptide

<400> 12
Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Ala Ala Gly
1 5 10 15

Val His Cys

<210> 13
<211> 642
<212> DNA
<213> Artificial sequence

<220>
<223> Mature light chain sequence

<220>
<221> CDS
<222> (1)..(642)

<400> 13
gag atc gtg ctc acg cag tct cca ggc acc ctg tct ttg tcg cca ggg 48
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

gaa cgt gcc acc ctc tcc tgc cgg gcc agt cag tcc gtt tcc agc gcg 96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ala
20 25 30

tac ctt gcc tgg tac cag cag aag cct ggc caa gct ccc agg ctc ctc 144
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

atc tat ggt gcg tcc agc agg gct act ggc att cca gac cgc ttc tca 192

Ile	Tyr	Gly	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Ile	Pro	Asp	Arg	Phe	Ser		
50						55					60						
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Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu		
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<211> 16
<212> PRT
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<220>
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<400> 18

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<210> 19
<211> 122
<212> PRT
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<220>
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<400> 19

Leu	Glu	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ser	Ser	Val	Lys
1				5					10					15	

Val	Ser	Cys	Lys	Ala	Ser	Gly	Gly	Ser	Phe	Ser	Ser	Tyr	Ala	Ile	Asn
			20					25					30		

Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	Gly	Gly	Leu
		35					40					45			

Met	Pro	Ile	Phe	Gly	Thr	Thr	Asn	Tyr	Ala	Gln	Lys	Phe	Gln	Asp	Arg
	50					55					60				

Leu	Thr	Ile	Thr	Ala	Asp	Val	Ser	Thr	Ser	Thr	Ala	Tyr	Met	Gln	Leu
65					70					75				80	

Ser	Gly	Leu	Thr	Tyr	Glu	Asp	Thr	Ala	Met	Tyr	Tyr	Cys	Ala	Arg	Val
				85					90					95	

Ala	Tyr	Met	Leu	Glu	Pro	Thr	Val	Thr	Ala	Gly	Gly	Leu	Asp	Val	Trp
			100					105					110		

Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ala	Ser
	115						120		

<210> 20

<211> 18
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<220>
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<400> 20

Asp Leu Leu Leu Gly Ser Glu Ala Asn Leu Thr Cys Thr Leu Thr Gly
1 5 10 15

Leu Arg

<210> 21
<211> 18
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<213> Artificial sequence

<220>
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<400> 21

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg

<210> 22
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> peptide tryptic fragment L-T2

<400> 22

Ala Thr Leu Ser Cys Arg
1 5

<210> 23
<211> 22
<212> PRT
<213> Artificial sequence

<220>
<223> peptide tryptic fragment L-T3

<400> 23

Ala Ser Gln Ser Val Ser Ser Ala Tyr Leu Ala Trp Tyr Gln Gln Lys
1 5 10 15

Pro Gly Gln Ala Pro Arg
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<210> 24

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> peptide tryptic fragment L-T4

<400> 24

Leu Leu Ile Tyr Gly Ala Ser Ser Arg
1 5

<210> 25

<211> 7

<212> PRT

<213> Artificial sequence

<220>

<223> peptide tryptic fragment L-T5

<400> 25

Ala Thr Gly Ile Pro Asp Arg
1 5

<210> 26

<211> 16

<212> PRT

<213> Artificial sequence

<220>

<223> peptide tryptic fragment L-T6

<400> 26

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg
1 5 10 15

<210> 27

<211> 16

<212> PRT

<213> Artificial sequence

<220>

<223> peptide tryptic fragment L-T7

<400> 27

Leu	Glu	Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	Gly	Arg
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<210> 28

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> peptide tryptic fragment L-T8

<400> 28

Ser	Pro	Thr	Phe	Gly	Gln	Gly	Thr	Lys
1				5				

<210> 29

<211> 18

<212> PRT

<213> Artificial sequence

<220>

<223> peptide tryptic fragment L-T11

<400> 29

Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln
1				5				10						15	

Leu Lys

<210> 30

<211> 16

<212> PRT

<213> Artificial sequence

<220>

<223> peptide tryptic fragment L-T12

<400> 30

Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg
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<210> 31

<211> 4

<212> PRT
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<220>
<223> peptide tryptic fragment L-T14

<400> 31

Val Gln Trp Lys
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<210> 32
<211> 20
<212> PRT
<213> Artificial sequence

<220>
<223> peptide tryptic fragment L-T15

<400> 32

Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu
1 5 10 15

Gln Asp Ser Lys
20

<210> 33
<211> 14
<212> PRT
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<220>
<223> peptide tryptic fragment L-T16

<400> 33

Asp Ser Thr Tyr Ser Leu Ser Asn Thr Leu Thr Leu Ser Lys
1 5 10

<210> 34
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> peptide tryptic fragment L-T17

<400> 34

Ala Asp Tyr Glu Lys
1 5

<210> 35
<211> 12
<212> PRT
<213> Artificial sequence

<220>
<223> peptide tryptic fragment L-T19

<400> 35

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Arg
1 5 10

<210> 36
<211> 5
<212> PRT
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<220>
<223> peptide tryptic fragment L-T20

<400> 36

Ser Pro Val Thr Lys
1 5

<210> 37
<211> 4
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<220>
<223> peptide tryptic fragment L-T21

<400> 37

Ser Phe Asn Arg
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<210> 38
<211> 23
<212> PRT
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<220>
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<400> 38

Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
1 5 10 15

Phe Thr Leu Thr Ile Ser Arg
20

<210> 39
<211> 32
<212> PRT
<213> Artificial sequence

<220>
<223> peptide tryptic fragment L-T6-7

<400> 39

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg
1 5 10 15

Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Arg
20 25 30

<210> 40
<211> 13
<212> PRT
<213> Artificial sequence

<220>
<223> peptide tryptic fragment L-T8-9

<400> 40

Ser Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
1 5 10

<210> 41
<211> 19
<212> PRT
<213> Artificial sequence

<220>
<223> peptide tryptic fragment L-T10-11

<400> 41

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1 5 10 15

Gln Leu Lys

<210> 42
<211> 19
<212> PRT

<213> Artificial sequence

<220>

<223> peptide tryptic fragment L-T12-13

<400> 42

Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg
1				5				10						15	

Glu Ala Lys

<210> 43

<211> 7

<212> PRT

<213> Artificial sequence

<220>

<223> peptide tryptic fragment L-T13-14

<400> 43

Glu	Ala	Lys	Val	Gln	Trp	Lys
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<210> 44

<211> 24

<212> PRT

<213> Artificial sequence

<220>

<223> peptide tryptic fragment L-T14-15

<400> 44

Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu
1				5				10						15	

Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys
			20				

<210> 45

<211> 7

<212> PRT

<213> Artificial sequence

<220>

<223> peptide tryptic fragment L-T17-18

<400> 45

Ala Asp Tyr Glu Lys His Lys
1 5

<210> 46
<211> 14
<212> PRT
<213> Artificial sequence

<220>
<223> peptide tryptic fragment L-T18-19

<400> 46

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Arg
1 5 10

<210> 47
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<223> peptide tryptic fragment L-T20-21

<400> 47

Ser Pro Val Thr Lys Ser Phe Asn Arg
1 5

<210> 48
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> peptide tryptic fragment L-T21-22

<400> 48

Ser Phe Asn Arg Gly Glu Cys
1 5

<210> 49
<211> 12
<212> PRT
<213> Artificial sequence

<220>
<223> peptide tryptic fragment H-T1

<400> 49

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys

1 5 10

<210> 50
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> peptide tryptic fragment H-T2

<400> 50

Lys Pro Gly Ser Ser Val Lys
1 5

<210> 51
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> peptide tryptic fragment H-T4

<400> 51

Ala Ser Gly Gly Ser Phe Ser Ser Tyr Ala Ile Asn Trp Val Arg
1 5 10 15

<210> 52
<211> 25
<212> PRT
<213> Artificial sequence

<220>
<223> peptide tryptic fragment H-T5

<400> 52

Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Gly Leu Met Pro Ile
1 5 10 15

Phe Gly Thr Thr Asn Tyr Ala Gln Lys
20 25

<210> 53
<211> 4
<212> PRT
<213> Artificial sequence

<220>
<223> peptide tryptic fragment H-T6

<400> 53

Phe Gln Asp Arg
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<210> 54

<211> 31

<212> PRT

<213> Artificial sequence

<220>

<223> peptide tryptic fragment H-T7

<400> 54

Leu Thr Ile Thr Ala Asp Val Ser Thr Ser Thr Ala Tyr Met Gln Leu
1 5 10 15

Ser Gly Leu Thr Tyr Glu Asp Thr Ala Met Tyr Tyr Cys Ala Arg
20 25 30

<210> 55

<211> 34

<212> PRT

<213> Artificial sequence

<220>

<223> peptide tryptic fragment H-T8

<400> 55

Val Ala Tyr Met Leu Glu Pro Thr Val Thr Ala Gly Gly Leu Asp Val
1 5 10 15

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Pro Thr Ser
20 25 30

Pro Lys

<210> 56

<211> 44

<212> PRT

<213> Artificial sequence

<220>

<223> peptide tryptic fragment H-T9

<400> 56

Val Phe Pro Leu Ser Leu Cys Ser Thr Gln Pro Asp Gly Asn Val Val

1 5 10 15

Ile Ala Cys Leu Val Gln Gly Phe Phe Pro Gln Glu Pro Leu Ser Val
20 25 30

Thr Trp Ser Glu Ser Gly Gln Gly Val Thr Ala Arg
35 40

<210> 57
<211> 30
<212> PRT
<213> Artificial sequence

<220>
<223> peptide tryptic fragment H-T10

<400> 57

Asn Phe Pro Pro Ser Gln Asp Ala Ser Gly Asp Leu Tyr Thr Thr Ser
1 5 10 15

Ser Gln Leu Thr Leu Pro Ala Thr Gln Cys Leu Ala Gly Lys
20 25 30

<210> 58
<211> 7
<212> PRT
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<220>
<223> peptide tryptic fragment H-T11

<400> 58

Ser Val Thr Cys His Val Lys
1 5

<210> 59
<211> 38
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<220>
<223> peptide tryptic fragment H-T12

<400> 59

His Tyr Thr Asn Pro Ser Gln Asp Val Thr Val Pro Cys Pro Val Pro
1 5 10 15

Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro
20 25 30

Ser Cys Cys His Pro Arg
35

<210> 60
<211> 27
<212> PRT
<213> Artificial sequence

<220>
<223> peptide tryptic fragment H-T13

<400> 60

Leu Ser Leu His Arg Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu
1 5 10 15

Ala Asn Leu Thr Cys Thr Leu Thr Gly Leu Arg
20 25

<210> 61
<211> 15
<212> PRT
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<400> 61

Asp Ala Ser Gly Val Thr Phe Thr Trp Thr Pro Ser Ser Gly Lys
1 5 10 15

<210> 62
<211> 9
<212> PRT
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<220>
<223> peptide tryptic fragment H-T15

<400> 62

Ser Ala Val Gln Gly Pro Pro Glu Arg
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<210> 63
<211> 23
<212> PRT

<213> Artificial sequence

<220>

<223> peptide tryptic fragment H-T16

<400> 63

Asp	Leu	Cys	Gly	Cys	Tyr	Ser	Val	Ser	Ser	Val	Leu	Pro	Gly	Cys	Ala
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Glu	Pro	Trp	Asn	His	Gly	Lys
			20			

<210> 64

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> peptide tryptic fragment H-T17

<400> 64

Thr	Phe	Thr	Cys	Thr	Ala	Ala	Tyr	Pro	Glu	Ser	Lys
1			5					10			

<210> 65

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> peptide tryptic fragment H-T18

<400> 65

Thr	Pro	Leu	Thr	Ala	Thr	Leu	Ser	Lys
1			5					

<210> 66

<211> 32

<212> PRT

<213> Artificial sequence

<220>

<223> peptide tryptic fragment H-T19

<400> 66

Ser	Gly	Asn	Thr	Phe	Arg	Pro	Glu	Val	His	Leu	Leu	Pro	Pro	Pro	Ser
1				5				10						15	

Glu Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu Ala Arg
20 25 30

<210> 67
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> peptide tryptic fragment H-T20

<400> 67

Gly Phe Ser Pro Lys
1 5

<210> 68
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> peptide tryptic fragment H-T21

<400> 68

Asp Val Leu Val Arg
1 5

<210> 69
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Thr Ile Asp Arg
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Val Asp Gly Thr Cys Tyr
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Ser Val Lys

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